

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/010,873A
Source: 1Fw16
Date Processed by STIC: 4/29/05

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 04/29/2005

PATENT APPLICATION: US/10/010,873A

TIME: 12:05:18

Input Set : A:\Revised sequence listing 2.txt

Output Set: N:\CRF4\04292005\J010873A.raw

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3 <110> APPLICANT: Medical Research Company
4     Sattlle, David
5     Culetto, Emmanuel
6     Baylis, Howard
8 <120> TITLE OF INVENTION: Recombinant Nematode Nicotinic Receptor and Uses
10 <130> FILE REFERENCE: 18396/2112
12 <140> CURRENT APPLICATION NUMBER: US 10/010,873A
13 <141> CURRENT FILING DATE: 2001-12-07
15 <150> PRIOR APPLICATION NUMBER: PCT/GB00/02270
16 <151> PRIOR FILING DATE: 2000-06-09
18 <150> PRIOR APPLICATION NUMBER: GB 9913248.2
19 <151> PRIOR FILING DATE: 1999-06-09
22 <160> NUMBER OF SEQ ID NOS: 4
24 <170> SOFTWARE: PatentIn Ver. 3.3
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 502
28 <212> TYPE: PRT
29 <213> ORGANISM: Caenorhabditis elegans
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34   1           5           10           15
36 Leu Ser Pro Pro Thr His Ala Asn Arg Asp Ala Asn Arg Leu Phe Glu
37           20           25           30
39 Asp Leu Ile Ala Asp Tyr Asn Lys Leu Val Arg Pro Val Ser Glu Asn
40           35           40           45
42 Gly Glu Thr Leu Val Val Thr Phe Lys Leu Lys Leu Ser Gln Leu Leu
43           50           55           60
45 Asp Val His Glu Lys Asn Gln Ile Met Thr Thr Asn Val Trp Leu Gln
46   65           70           75           80
48 His Ser Trp Met Asp Tyr Lys Leu Arg Trp Asp Pro Val Glu Tyr Gly
49           85           90           95
51 Gly Val Glu Val Leu Tyr Val Pro Ser Asp Thr Ile Trp Leu Pro Asp
52           100          105          110
54 Val Val Leu Tyr Asn Asn Ala Asp Gly Asn Tyr Gln Val Thr Ile Met
55           115          120          125
57 Thr Lys Ala Lys Leu Thr Tyr Asn Gly Thr Val Glu Trp Ala Pro Pro
58           130          135          140
60 Ala Ile Tyr Lys Ser Met Cys Gln Ile Asp Val Glu Phe Phe Pro Phe
61   145          150          155          160
63 Asp Arg Gln Gln Cys Glu Met Lys Phe Gly Ser Trp Thr Tyr Gly Gly
64           165          170          175
66 Leu Glu Val Asp Leu Gln His Arg Asp Lys His Leu Glu Lys Glu Ile
67           180          185          190

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69 Glu Glu Asp Val Glu Gly Val Asp Gly Pro Thr Lys Glu Ile Val Trp
70      195      200      205
72 Val Val Asp Arg Gly Ile Asp Leu Ser Asp Tyr Tyr Pro Ser Val Glu
73      210      215      220
75 Trp Asp Ile Leu Asn Val Pro Gly Lys Arg His Ser Lys Arg Tyr Pro
76 225      230      235      240
78 Cys Cys Glu Ser Pro Phe Ile Asp Ile Thr Tyr Glu Ile His Leu Arg
79      245      250      255
81 Arg Lys Thr Leu Phe Tyr Thr Val Asn Leu Ile Phe Pro Ser Val Gly
82      260      265      270
84 Ile Ser Phe Leu Thr Ala Leu Val Phe Tyr Leu Pro Ser Asp Gly Gly
85      275      280      285
87 Glu Lys Ile Ser Leu Cys Ile Ser Ile Leu Ile Ser Leu Thr Val Phe
88      290      295      300
90 Phe Leu Leu Leu Val Glu Ile Ile Pro Ser Thr Ser Leu Val Ile Pro
91 305      310      315      320
93 Leu Ile Gly Lys Tyr Leu Leu Phe Thr Met Val Leu Val Thr Leu Ser
94      325      330      335
96 Val Val Val Thr Val Val Thr Leu Asn Val His Tyr Arg Ser Pro Thr
97      340      345      350
99 Thr His Thr Met Pro Lys Trp Met Lys Arg Leu Phe Val Asp Phe Leu
100      355      360      365
102 Pro Lys Tyr Leu Leu Met Thr Arg Pro Gln Pro Pro Gly His His Ser
103      370      375      380
105 Lys Pro Asn Arg Lys Phe Asp Ser Arg Ala Ser Thr Phe Ser Ile Gly
106 385      390      395      400
108 Val Asn His Val Leu Gly Gln Asn Ser Glu Leu Leu Ser Pro Gly Leu
109      405      410      415
111 Asn Ser Asn Arg Glu Glu Ser Ser Phe Thr Leu Pro Arg Asp Asn Ser
112      420      425      430
114 Pro Val Arg Ser Ala Val Glu Ser Val Ala Tyr Ile Ala Asp His Leu
115      435      440      445
117 Lys Asn Glu Glu Asp Asp Lys Gln Val Ile Glu Asp Trp Lys Tyr Ile
118      450      455      460
120 Ser Val Val Met Asp Arg Ile Phe Leu Ile Thr Phe Thr Phe Ala Cys
121 465      470      475      480
123 Ala Phe Gly Thr Val Val Ile Ile Ala Arg Ala Pro Ser Ile Tyr Asp
124      485      490      495
126 Asn Thr Pro Ala Leu Ala
127      500
130 <210> SEQ ID NO: 2
131 <211> LENGTH: 513
132 <212> TYPE: PRT
133 <213> ORGANISM: Caenorhabditis elegans
135 <220> FEATURE:
136 <221> NAME/KEY: MISC_FEATURE
137 <222> LOCATION: (86)..(109); (206)..(225); (322)..(345); (430)..(452)
138 <223> OTHER INFORMATION: Xaa at these positions can be any amino acid.
140 <400> SEQUENCE: 2

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141 Met Arg Ser Phe Trp Leu Phe Leu Leu Leu Leu Phe Cys Ile Ser
142 1 5 10 15
144 Phe Ile Lys Leu Thr Glu Gly Asn Glu Asp Ala Lys Arg Leu Tyr Asp
145 20 25 30
147 Asp Leu Met Val Asn Tyr Asn Arg His Arg Arg Pro Ser Thr Ser Pro
148 35 40 45
150 Asn Lys Pro Leu Thr Ile Lys Leu Lys Leu Lys Leu Arg Leu Ser Gln
151 50 55 60
153 Ile Ile Asp Val His Glu Ile Asp Gln Ile Met Thr Cys Ser Val Trp
154 65 70 75 80
W--> 156 Leu Lys Gln Thr Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
157 85 90 95
159 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
160 100 105 110
162 Pro Asp Ile Val Leu Tyr Asn Asn Ala Asp Ser Asn Tyr Asn Ile Thr
163 115 120 125
165 Ile Ser Thr Lys Ala Thr Leu His Tyr Thr Gly Glu Val Thr Trp Glu
166 130 135 140
168 Pro Pro Ala Ile Phe Lys Ser Met Cys Gln Ile Asp Val Arg Trp Phe
169 145 150 155 160
171 Pro Phe Asp Glu Gln Gln Cys His Leu Lys Phe Gly Ser Trp Thr Phe
172 165 170 175
174 Ser Glu Asn Leu Leu Ser Val Glu Leu Asn Glu Pro Ser Leu Arg Tyr
175 180 185 190
177 Glu Glu Glu Ile Asp Glu Lys Gly Ile Ile Asp Asn Val Xaa Xaa Xaa
178 195 200 205
180 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
181 210 215 220
183 Xaa Met Ser Arg Val Ala Lys Arg Arg Ala Lys Asn Tyr Pro Ser Cys
184 225 230 235 240
186 Cys Pro Gln Ser Ala Tyr Ile Asp Val Thr Tyr Tyr Leu Gln Leu Arg
187 245 250 255
189 Arg Lys Pro Leu Phe Tyr Thr Val Asn Leu Val Phe Pro Cys Val Gly
190 260 265 270
192 Ile Ser Phe Leu Thr Ile Leu Val Phe Tyr Leu Pro Ser Asp Ser Gly
193 275 280 285
195 Glu Lys Val Thr Leu Cys Ile Ser Ile Leu Val Ala Leu Thr Ile Phe
196 290 295 300
198 Phe Leu Leu Leu Thr Glu Ile Ile Pro Ala Thr Ser Ile Thr Leu Pro
199 305 310 315 320
201 Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
202 325 330 335
204 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
205 340 345 350
207 Thr His Leu Met Pro Asn Trp Val Lys Lys Val Phe Leu Lys Trp Leu
208 355 360 365
210 Pro Lys Leu Leu Phe Met Arg Arg Pro Ile Asp Asp Tyr Glu Glu Lys
211 370 375 380
213 Phe Asp Asp Lys Lys Lys Pro Lys Asp Gly Lys Ile Ala Leu Ser Val

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214 385          390          395          400
216 His Ala His Arg Val Ser Asn Val Gly Asn Asn Ile Arg Asn Ala Thr
217          405          410          415
219 Ile Asp Asp Thr Ile Gln Lys Met Tyr Tyr Ser Pro Pro Xaa Xaa Xaa
220          420          425          430
222 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
223          435          440          445
225 Xaa Xaa Xaa Xaa Ile Asp Glu Asp Trp Lys Tyr Val Ala Met Val Leu
226          450          455          460
228 Asp Arg Leu Phe Leu Leu Ile Phe Ser Ile Ala Cys Phe Val Gly Thr
229 465          470          475          480
231 Val Ile Ile Leu Leu Arg Ala Pro Thr Leu Tyr Asp Thr Arg Gln Pro
232          485          490          495
234 Ile Asp Leu Gln Tyr Arg Pro Ala Asn Leu Ser Ala Asn Pro Ile Ser
235          500          505          510
237 Phe
240 <210> SEQ ID NO: 3
241 <211> LENGTH: 507
242 <212> TYPE: PRT
243 <213> ORGANISM: Caenorhabditis elegans
244 <220> FEATURE:
245 <221> NAME/KEY: MISC_FEATURE
246 <222> LOCATION: (96)..(119); (196)..(214); (301)..(324); (417)..(439)
247 <223> OTHER INFORMATION: Xaa at these positions can be any amino acid.
250 <400> SEQUENCE: 3
251 Met Met Leu Gly Gly Gly Gly Gly Cys Gly Ala Gly Gly Thr Trp Leu
252 1          5          10          15
254 Gly Phe Leu Val Phe Leu Ala Val Ser Leu Arg Asn His Ser Thr Cys
255          20          25          30
257 Glu Asp Ile Asp Ala Glu Asp Arg Leu Met Val Asp Leu Phe Arg Gly
258          35          40          45
260 Tyr Asn Ser Leu Val Gln Pro Val Arg Asn Arg Ser Glu Leu Pro Met
261          50          55          60
263 Ile Val Lys Ile Gly Met Gln Leu Val Leu Leu Ile Asn Val Asp Glu
264 65          70          75          80
W--> 266 Lys Glu Gln Val Met His Thr Asn Val Trp Leu Thr Met Lys Trp Xaa
267          85          90          95
269 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
270          100          105          110
272 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Trp Leu Pro Asp Ile Val Leu Phe
273          115          120          125
275 Asn Asn Ala Asp Gly Asn Tyr Glu Val Ser Phe Met Cys Asn Val Leu
276          130          135          140
278 Ile Leu Ser Thr Gly Thr Val Leu Trp Val Pro Pro Ala Ile Tyr Lys
279 145          150          155          160
281 Ser Ser Cys Ile Ile Asp Val Glu Phe Phe Pro Phe Asp Asp Gln Leu
282          165          170          175
284 Cys Ser Leu Thr Phe Gly Ser Trp Thr Tyr Asn Arg Asp Glu Ile Lys
285          180          185          190

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287 Leu Asp Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
288      195      200      205
290 Xaa Xaa Xaa Xaa Xaa Xaa Met Asp Gly Pro Ala Val Leu Thr Ser Asp
291      210      215      220
293 Arg Ser Arg Ile Glu Phe Gln Ile Arg Ile Arg Arg Lys Thr Leu Phe
294 225      230      235      240
296 Tyr Thr Val Val Leu Ile Leu Pro Thr Val Leu Met Ala Phe Leu Asn
297      245      250      255
299 Val Thr Val Phe Tyr Leu Pro Thr Ala Ser Gly Glu Lys Met Gly Leu
300      260      265      270
302 Thr Met Asn Val Leu Leu Ser Ile Val Val Phe Leu Leu Leu Val Ser
303      275      280      285
305 Lys Ile Leu Pro Pro Thr Ser Ser Ser Ile Pro Leu Xaa Xaa Xaa Xaa
306      290      295      300
308 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
309 305      310      315      320
311 Xaa Xaa Xaa Xaa Ile Tyr Phe Arg Ser Pro Ile Thr His Arg Leu Pro
312      325      330      335
314 Pro Trp Val Arg Lys Val Phe Leu Asp Ile Leu Pro Leu Leu Met Cys
315      340      345      350
317 Met Gln Arg Pro His Arg Lys Asn Val Ile Gln Arg Ser His Arg Arg
318      355      360      365
320 Leu Leu Glu Thr Gly Pro Ser Val Glu Glu Asn Pro Met Arg Ser Gly
321      370      375      380
323 Glu His His Pro Leu Cys Arg His Thr His Asn Gln Asp Ser Cys Arg
324 385      390      395      400
326 Arg Val Arg Ile Gln Ser Asp Glu Leu Asp Asp Glu Leu Ser Pro Glu
327      405      410      415
329 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
330      420      425      430
332 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Arg Asp Asp Trp Lys Phe Ile Ala
333      435      440      445
335 Ser Val Val Asp Arg Phe Leu Leu Tyr Gly Phe Phe Gly Ala Thr Val
336      450      455      460
338 Gly Gly Thr Ile Gly Ile Ile Phe Thr Ala Pro Ser Val Phe Glu Thr
339 465      470      475      480
341 Phe Asp Glu Asn Ala Thr Leu Val Lys Leu Lys Gln Leu Tyr Asp Met
342      485      490      495
344 Gly Leu Ala Asn Asp Thr Val Leu Gly Ile Phe
345      500      505
348 <210> SEQ ID NO: 4
349 <211> LENGTH: 493
350 <212> TYPE: PRT
351 <213> ORGANISM: Caenorhabditis elegans
353 <220> FEATURE:
354 <221> NAME/KEY: MISC_FEATURE
355 <222> LOCATION: (88)..(111); (188)..(206); (292)..(316); (409)..(431)
356 <223> OTHER INFORMATION: Xaa at these positions can be any amino acid.
358 <400> SEQUENCE: 4

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RAW SEQUENCE LISTING ERROR SUMMARY
 PATENT APPLICATION: US/10/010,873A

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Input Set : A:\Revised sequence listing 2.txt
 Output Set: N:\CRF4\04292005\J010873A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; Xaa Pos. ~~86,87,88,89,90,91,92,93,94,95,96,97,98,99,100,101,102,103~~
 Seq#:2; Xaa Pos. ~~104,105,106,107,108,109,206,207,208,209,210,211,212,213~~
 Seq#:2; Xaa Pos. ~~214,215,216,217,218,219,220,221,222,223,224,225,322,323~~
 Seq#:2; Xaa Pos. ~~324,325,326,327,328,329,330,331,332,333,334,335,336,337~~
 Seq#:2; Xaa Pos. ~~338,339,340,341,342,343,344,345,430,431,432,433,434,435~~
 Seq#:2; Xaa Pos. ~~436,437,438,439,440,441,442,443,444,445,446,447,448,449~~
 Seq#:2; Xaa Pos. ~~450,451,452~~
 Seq#:3; Xaa Pos. ~~96,97,98,99,100,101,102,103,104,105,106,107,108,109,110~~
 Seq#:3; Xaa Pos. ~~111,112,113,114,115,116,117,118,119,196,197,198,199,200~~
 Seq#:3; Xaa Pos. ~~201,202,203,204,205,206,207,208,209,210,211,212,213,214~~
 Seq#:3; Xaa Pos. ~~301,302,303,304,305,306,307,308,309,310,311,312,313,314~~
 Seq#:3; Xaa Pos. ~~315,316,317,318,319,320,321,322,323,324,417,418,419,420~~
 Seq#:3; Xaa Pos. ~~421,422,423,424,425,426,427,428,429,430,431,432,433,434~~
 Seq#:3; Xaa Pos. ~~435,436,437,438,439~~
 Seq#:4; Xaa Pos. ~~88,89,90,91,92,93,94,95,96,97,98,99,100,101,102,103,104~~
 Seq#:4; Xaa Pos. ~~105,106,107,108,109,110,111,188,189,190,191,192,193,194~~
 Seq#:4; Xaa Pos. ~~195,196,197,198,199,200,201,202,203,204,205,206,292,293~~
 Seq#:4; Xaa Pos. ~~294,295,296,297,298,299,300,301,302,303,304,305,306,307~~
 Seq#:4; Xaa Pos. ~~308,309,310,311,312,313,314,315,316,409,410,411,412,413~~
 Seq#:4; Xaa Pos. ~~414,415,416,417,418,419,420,421,422,423,424,425,426,427~~
 Seq#:4; Xaa Pos. ~~428,429,430,431~~

VERIFICATION SUMMARY

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TIME: 12:05:19

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L:156 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:80
M:341 Repeated in SeqNo=2
L:266 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:80
M:341 Repeated in SeqNo=3
L:374 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:80
M:341 Repeated in SeqNo=4